

What is claimed is

1. An automated method for simulating a biological network, said method comprising:
  - a) receiving initial condition values, process parameters, and a user representation of the biological network, wherein the user representation is input using one or more of a series of biological network canonical input forms, wherein each canonical input form is based on a type of biological process in the biological network;
  - b) generating a series of mathematical equations in an equation output canonical form based on the input representation of the biological network and the process parameters; and
  - c) numerically solving the series of mathematical equations using the initial condition values and the process parameters, to generate a value or a table of values as a function of time for one or more output functions of the biological network, thereby simulating the biological network.
2. The method of claim 1, wherein the series of mathematical equations are a series of differential equations.
3. The method of claim 1, further comprising manually modifying the series of mathematical equations before solving the series of mathematical equations.
4. The method of claim 1, wherein the generating a series of mathematical equations comprises generating a hierarchical arrangement of canonical input forms and associated canonical output forms from the input representation and the process parameters, wherein a level of the hierarchical arrangement comprises the series of mathematical equations.

5. The method of claim 4, wherein the canonical output forms are modifiable by a user at each level of the hierarchical arrangement.

6. The method of claim 1, wherein the user representation of the biological network is a series of graphics of a graphic user interface.

7. The method of claim 1, wherein the method further comprises before generating a series of mathematical equations, generating a series of chemical equation canonical input forms based on a more detailed representation of the biological network than the user representation of the biological network.

8. The method of claim 7, wherein the biological network comprises a regulatory cascade, and wherein the automated method is implemented using a computer algebra program.

9. The method of claim 1, further comprising repeating steps a-c after changing one or both the initial condition values and the representation of the biological network, and analyzing the affect of the changes on value or table of values of the one or more output functions.

10. The method of claim 9, wherein the changes are based on the biological activity of an on-test reagent.

11. The method of claim 9 wherein the biological network is a dynamic network and wherein the changes are based on the one or more output functions reached during a preceding cycle of steps a-c.

12. The method of claim 9, wherein steps a-c are repeated until a predefined end time point has been reached.

13. The method of claim 9, further comprising defining a target output value and recording the input conditions that achieve this target output value, wherein the changes are automatically generated and steps a-c are automatically repeated until the target output value is attained.

14. The method of claim 1, wherein the biological process comprises a biochemical process having a linear pathway mediated by sequential biochemical modification.

15. The method of claim 4, wherein the biological network is a developmental network and the methods use domains and fields for representing the biological network.

16. The method of claim 4, wherein the biological network comprises a developmental network.

17. The method of claim 4, wherein the method provides a representation of an organism as a graph, wherein the graph comprises a list of nodes representing cells, a list of links of the cells, and a lineage tree of the cells.

18. The method of claim 4, wherein each node comprises one or more models comprising a system of differential equations and associated parameters that described some aspect of the biological network.

19. A computer system comprising:  
a user interface capable of receiving and displaying initial condition values, process parameters, and a user representation of a biological network, wherein the user

representation is input as a series of canonical input forms, wherein the format for each canonical input form is based on a type of biological process in the biological network;

an interpreter function capable of generating a hierarchical arrangement of canonical input forms and associated canonical output forms from the input representation and the process parameters, wherein a level of the hierarchical arrangement comprises a series of differential equations; and

an equation solver function capable of receiving the process parameters, the initial condition values, and the series of differential equations, and numerically solving the differential equations, thereby generating a value or a table of values as a function of time for one or more output functions.

20. The computer system of claim 19, wherein the user interface displays the canonical output forms at every level to allow a user to modify the canonical output forms.

21. The computer system of claim 19, further comprising a graphing function capable of generating a graph of the value or table of values.

22. The computer system of claim 19, further comprising a graphing function that graphs the relationship of cells in a developmental system using the solved differential equation.

23. A method for generating revenue comprising providing access to the computer system of claim 19 for a fee.

24. A computer program product for simulating a biological network comprising a computer-usable medium having a computer-readable program code for effecting the following steps within a computing system:

a) receiving initial condition values, process parameters, and a user representation of the biological network, wherein the user representation is input using one or more of a series of biological network canonical input forms, wherein the format for each canonical input form is based on a type of biological process in the biological network;

b) generating a hierarchical arrangement of canonical input forms and associated canonical output forms from the input representation and the process parameters, wherein a level of the hierarchical arrangement comprises a series of differential equations; and

c) numerically solving the differential equations to generate a value or a table of values as a function of time for one or more output functions of the biological network by inputting the initial condition values and the process parameters into the solved mathematical equation, thereby simulating the biological network.

25. The computer program of claim 24, wherein the canonical output forms are modifiable by a user at each level of the hierarchical arrangement.

26. The computer program of claim 24, wherein the biological network is a developmental network.

27. The computer program of claim 26, wherein the computer program further effects representing a developmental network of an organism as a graph, wherein the graph comprises a list of nodes representing cells, a list of links of the cells, and a lineage tree of the cells.

28. An automated method for simulating a developmental process of an organism, said method comprising:

a) receiving initial condition values and process parameters for the developmental process of the organism;

b) representing the organism or a tissue within the organism by a graph data structure, wherein the graph data structure comprises:

i) a list of links, each link representing the interaction between two cells;

ii) a lineage tree recording the family tree of cell birth for the cells represented by the list of links; and

iii) a list of nodes, each node representing a cell of the cells represented by the list of links, with an embedding describing the location of the cell in Cartesian coordinates and a set of differential equations describing the time evolution of the location of the cell, said differential equations comprising the initial condition values and process parameters, each node comprising a model that comprises a system of differential equations and associated parameters describing the developmental process; and

c) repeatedly solving the set of differential equations in a series of steps for a defined number of steps, wherein after each step results are generated and compared to a threshold to determine whether the developmental process has reached a trigger point for changing the number of nodes in the list of nodes, thereby simulating the developmental process.

29. The method of claim 28, further comprising:

d) graphing the nodes using the Cartesian coordinates.

30. The method of claim 28, wherein the developmental process is cell division, wherein reaching the trigger point adds a new node to the list of nodes.

31. The method of claim 28, wherein the developmental process is cell death, wherein reaching the trigger point adds a new node to the list of nodes.

32. The method of claim 28, wherein the automated method is implemented using a computer algebra program.

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